



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number. 10/786,445

Source IFWO

Date Processed by STIC 3/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room HB03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/786,445

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence  
    (2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
    is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
    "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003



IFWO

## RAW SEQUENCE LISTING

DATE: 03/08/2004

PATENT APPLICATION: US/10/786,445

TIME: 15:16:40

Input Set : A:\Sequence Listing - Docket No. 096429-9141.txt

Output Set: N:\CRF4\03082004\J786445.raw

3 <110> APPLICANT: Welch, Rodney A.  
 4 Lathem, Wyndham W.  
 5 Grys, Thomas E.  
 7 <120> TITLE OF INVENTION: E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE  
 9 <130> FILE REFERENCE: 096429-9141  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/786,445  
 12 <141> CURRENT FILING DATE: 2004-02-25  
 14 <150> PRIOR APPLICATION NUMBER: 10/002,309  
 15 <151> PRIOR FILING DATE: 2001-10-26  
 17 <150> PRIOR APPLICATION NUMBER: 60/243,675  
 18 <151> PRIOR FILING DATE: 2000-10-26  
 20 <160> NUMBER OF SEQ ID NOS: 25  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2798  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Unknown  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid

Does Not Comply  
 Corrected Diskette Needed  
 (Pg. 7)

p0157

32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (138)..(2798)  
 35 <223> OTHER INFORMATION:  
 W--> 38 <400> 1  
 39 ttacgaaac aggtgtaaat atgttataaa aataaccaac gactagttaa taagtcgctc 60  
 41 ctgaaaaaat aaaatataga aataactgtta tatccgctg catgaacact aaaatgaatg 120  
 43 agagatggag aacacccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170  
 44 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
 45 1 5 10  
 47 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218  
 48 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
 49 15 20 25  
 51 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266  
 52 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
 53 30 35 40  
 55 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314  
 56 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
 57 45 50 55  
 59 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362  
 60 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
 61 60 65 70 75  
 63 agt ctg ctg ctt gtc cgt cgg gtg aaa gct gat gat aaa aca cct gtt 410  
 64 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val

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65	80	85	90	
67	cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc	458		
68	Gln Val Glu Ala Arg Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr			
69	95	100	105	
71	ctt tat cct cct tca tca cta cgc gat aca atc tac cat ctg gat ggt	506		
72	Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly			
73	110	115	120	
75	gtt cgc gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag	554		
76	Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys			
77	125	130	135	
79	atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg	602		
80	Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly			
81	140	145	150	
83	agt tct att cat agc cat cta aca aat aat gca ctg gtg gag atc cat	650		
84	Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His			
85	160	165	170	
87	act gca aat ggt cgt tgg gta aga gac att tat ctg cgc cag gga ccc	698		
88	Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro			
89	175	180	185	
91	gac ctt gaa ggt aag atg gtt cgc ttt gtt tgc tct gca ggc tat agt	746		
92	Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser			
93	190	195	200	
95	tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tgc gtg ggt aac	794		
96	Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn			
97	205	210	215	
99	act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa	842		
100	Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu			
101	220	225	230	
103	ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa	890		
104	Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu			
105	240	245	250	
107	ctg cct cgc cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag	938		
108	Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln			
109	255	260	265	
111	ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca cgc ggt	986		
112	Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly			
113	270	275	280	
115	gag ctg ttg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg	1034		
116	Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg			
117	285	290	295	
119	gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc	1082		
120	Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe			
121	300	305	310	
123	cag acc att cct gta agt cgt atg att gtt aat aat tat cgc cct cta	1130		
124	Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu			
125	320	325	330	
127	cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg	1178		
128	His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met			
129	335	340	345	

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131	gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
132	Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
133			350				355						360				
135	ggt	aaa	gaa	ttg	gtt	tcg	cat	ggc	att	gat	aat	gct	aac	tat	ggt	tta	1274
136	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
137			365				370					375					
139	aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcg	1322
140	Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
141			380				385					390				395	
143	caa	tta	gcg	gca	cat	aat	agc	cgc	ggt	aat	tat	gct	aat	ggc	atc	cag	1370
144	Gln	Leu	Ala	Ala	His	Asn	Ser	Arg	Gly	Asn	Tyr	Ala	Asn	Gly	Ile	Gln	
145						400					405				410		
147	gtt	cat	ggt	ggc	tcc	gga	ggt	ggg	gga	att	ggt	act	tta	gat	tcc	aca	1418
148	Val	His	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ile	Val	Thr	Leu	Asp	Ser	Thr	
149				415						420				425			
151	ttg	ggg	aat	gaq	ttc	agt	cat	gaa	gtt	ggt	cat	aat	tat	ggt	ctt	ggt	1466
152	Leu	Gly	Asn	Glu	Phe	Ser	His	Glu	Val	Gly	His	Asn	Tyr	Gly	Leu	Gly	
153			430				435					440					
155	cat	tat	gta	gat	ggt	ttc	aag	ggt	tct	gta	cat	cgt	agt	gca	gaa	aat	1514
156	His	Tyr	Val	Asp	Gly	Phe	Lys	Gly	Ser	Val	His	Arg	Ser	Ala	Glu	Asn	
157			445				450					455					
159	aac	aac	tca	act	tgg	gga	tgg	gat	ggt	gat	aaa	aaa	cgg	ttt	att	cct	1562
160	Asn	Asn	Ser	Thr	Trp	Gly	Trp	Asp	Gly	Asp	Lys	Lys	Arg	Phe	Ile	Pro	
161			460				465					470				475	
163	aac	ttt	tat	ccg	tct	caa	aca	aat	gaa	aag	agt	tgt	ctg	aat	aat	cag	1610
164	Asn	Phe	Tyr	Pro	Ser	Gln	Thr	Asn	Glu	Lys	Ser	Cys	Leu	Asn	Asn	Gln	
165				480						485				490			
167	tgt	caa	gaa	ccg	ttt	gat	gga	cac	aaa	ttt	ggt	ttt	gac	gcc	atg	gcg	1658
168	Cys	Gln	Glu	Pro	Phe	Asp	Gly	His	Lys	Phe	Gly	Phe	Asp	Ala	Met	Ala	
169				495						500				505			
171	gga	ggc	agc	cct	ttc	tct	gct	gca	aac	cgt	ttc	aca	atg	tat	act	ccg	1706
172	Gly	Gly	Ser	Pro	Phe	Ser	Ala	Ala	Asn	Arg	Phe	Thr	Met	Tyr	Thr	Pro	
173			510				515					520					
175	aat	tca	tcg	gct	atc	atc	cag	cgt	ttt	ttt	gaa	aat	aaa	gct	gtg	ttc	1754
176	Asn	Ser	Ser	Ala	Ile	Ile	Gln	Arg	Phe	Phe	Glu	Asn	Lys	Ala	Val	Phe	
177			525				530					535					
179	gat	agc	cgt	tcc	tcc	acc	ggc	ttc	agc	aag	tgg	aat	gca	gat	acg	cag	1802
180	Asp	Ser	Arg	Ser	Ser	Thr	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Asp	Thr	Gln	
181				540			545				550				555		
183	gaa	atg	gaa	ccg	tat	gaa	cac	acc	att	gac	cgt	gcg	gag	cag	att	acg	1850
184	Glu	Met	Glu	Pro	Tyr	Glu	His	Thr	Ile	Asp	Arg	Ala	Glu	Gln	Ile	Thr	
185				560			565					570					
187	gct	tca	gtc	aat	gag	cta	agt	gaa	agc	aaa	atg	gct	gag	ctg	atg	gca	1898
188	Ala	Ser	Val	Asn	Glu	Leu	Ser	Glu	Ser	Lys	Met	Ala	Glu	Leu	Met	Ala	
189				575			580					585					
191	gag	tac	gct	gtc	gtc	aaa	gtg	cat	atg	tgg	aac	ggt	aac	tgg	aca	aga	1946
192	Glu	Tyr	Ala	Val	Val	Lys	Val	His	Met	Trp	Asn	Gly	Asn	Trp	Thr	Arg	
193				590			595					600					
195	aac	atc	tat	atc	cct	aca	gcc	tcc	gca	gat	aat	aga	ggc	agt	atc	ctg	1994

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196 Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu
197      605      610      615
199 acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt      2042
200 Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly
201 620      625      630      635
203 gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat      2090
204 Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp
205      640      645      650
207 ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt      2138
208 Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg
209      655      660      665
211 aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac      2186
212 Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr
213      670      675      680
215 gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt      2234
216 Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly
217      685      690      695
219 gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac      2282
220 Ala Tyr Gly Phe Thr Tyr Ser Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn
221 700      705      710      715
223 gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga      2330
224 Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gln Leu Arg Phe Arg
225      720      725      730
227 ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att      2378
228 Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile
229      735      740      745
231 aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat      2426
232 Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn
233      750      755      760
235 aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt      2474
236 Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu
237      765      770      775
239 acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga      2522
240 Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly
241 780      785      790      795
243 tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt      2570
244 Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly
245      800      805      810
247 caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc      2618
248 Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val
249      815      820      825
251 tat gtc gac agc ggg gct aaa gcg aaa gtg ctt ctt gac tgg gat      2666
252 Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Ser Asp Trp Asp
253      830      835      840
255 aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca      2714
256 Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro
257      845      850      855
259 gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc      2762
260 Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe

```

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261 860 865 870 875 2798

263 agt aaa cct agg tca atg agg gtt gta tat aaa taa

264 Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys

265 880 885

268 <210> SEQ ID NO: 2

269 <211> LENGTH: 886

270 <212> TYPE: PRT

271 <213> ORGANISM: Unknown

273 <220> FEATURE:

274 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid

p0157

276 <400> SEQUENCE: 2

278 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile

279 1 5 10 15

282 Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe

283 20 25 30

286 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu

287 35 40 45

290 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly

291 50 55 60

294 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val

295 65 70 75 80

298 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg

299 85 90 95

302 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser

303 100 105 110

306 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly

307 115 120 125

310 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val

311 130 135 140

314 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser

315 145 150 155 160

318 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg

319 165 170 175

322 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys

323 180 185 190

326 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr

327 195 200 205

330 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys

331 210 215 220

334 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg

335 225 230 235 240

338 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp

339 245 250 255

342 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly

343 260 265 270

346 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His

347 275 280 285

350 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe

351 290 295 300

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/786,445

DATE: 03/08/2004

TIME: 15:16:41

Input Set : A:\Sequence Listing - Docket No. 096429-9141.txt

Output Set: N:\CRF4\03082004\J786445.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35  
L:658 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:655



US/10/786,445

Page 7 of 7

<210> SEQ ID NO 4  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Synthetic Oligonucleotide  
<400> SEQUENCE: 4  
ccctcgagtt tacgaacag gtgtaaat

Per new Sequence Rules,  
<213> response has to  
be either

Artificial/Unknown<sup>28</sup>  
or Genus/Species.

please see  
item # 10

on error  
Summary  
Sheet.

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.